

Whole-exome sequencing results

All WES samples are downloaded from <ftp://ftp.1000genomes.ebi.ac.uk>. Like we did on retinitis pigmentosa dataset, considering multiple factors such as DNA quality, DNA extraction protocol and the possibly non-even reads distribution, we randomly selected three samples to pool together as control (NA19152, NA18973 and NA19206NA), and one sample as case (NA10847). We performed SeqCNV on chromosome 1 of these samples. To test performance of SeqCNV on WES data, we validate results of SeqCNV with the CNVs previously reported by Conrad et al. (PMID: 19812545) in the WES samples.

Control sample selection

On retinitis pigmentosa patient data, for CoNIFER andXHMM, we added extra 46 samples without copy change in *PRPF31* as control due the requirement of SVD and PCA methods. These 46 samples are normal samples and we selected them as controls for RP samples based on the following reasons:

- 1) Their DNA quality is good and the DNA extraction methods of these 46 and RP samples are the same.
- 2) The 46 normal samples and RP samples are designed to cover the same genomic regions and their number of sequencing reads are also similar.
- 3) The 46 normal samples and RP samples were sequenced in the same batch with RP samples.